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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/991,143*

DATE: 07/23/98
TIME: 14:43:16

INPUT SET: S27646.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
                              SEQUENCE LISTING

(1)    General Information:                   ENTERED

       (i) APPLICANT: Conti-Fine, B.M.

      (ii) TITLE OF INVENTION: PREVENTION OF EXPERIMENTAL MYASTHANIA GRAVIS

     (iii) NUMBER OF SEQUENCES: 2

      (iv) CORRESPONDENCE ADDRESS:
           (A) ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
           (B) STREET: 121 South Eigth Street, 1600 TCF Tower
           (C) CITY: Minneapolis
           (D) STATE: MN
           (E) COUNTRY: USA
           (F) ZIP: 55402

       (v) COMPUTER READABLE FORM:
           (A) MEDIUM TYPE: Diskette
           (B) COMPUTER: IBM Compatible
           (C) OPERATING SYSTEM: Windows 95
           (D) SOFTWARE: FastSEQ for Windows Version 2.0b

      (vi) CURRENT APPLICATION DATA:
           (A) APPLICATION NUMBER: 08/991,143
           (B) FILING DATE: 16-DEC-1997
           (C) CLASSIFICATION:

     (vii) PRIOR APPLICATION DATA:
           (A) APPLICATION NUMBER:
           (B) FILING DATE:



    (viii) ATTORNEY/AGENT INFORMATION:
           (A) NAME: Embretson, Janet E
           (B) REGISTRATION NUMBER: 39,665
           (C) REFERENCE/DOCKET NUMBER: 600.423US1

      (ix) TELECOMMUNICATION INFORMATION:
           (A) TELEPHONE: 612-373-6959
           (B) TELEFAX: 612-339-3061
           (C) TELEX:
```

47
48   (2) INFORMATION FOR SEQ ID NO:1:
49
50   (i) SEQUENCE CHARACTERISTICS:
51   (A) LENGTH: 1667 base pairs
52   (B) TYPE: nucleic acid
53   (C) STRANDEDNESS: single
54   (D) TOPOLOGY: linear
55
56   (ii) MOLECULE TYPE: cDNA
57
58   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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59  AAGCACAGGC CACCACTCTG CCCTGGTCCA CACAAGCTCC GGTAGCCCAT GGAGCCCTGG    60
60  CCTCTCCTCC TGCTCTTTAG CCTTTGCTCA GCTGGCCTCG TCCTGGGCTC CGAACATGAG   120
61  ACCCGTCTGG TGGCAAAGCT ATTTAAAGAC TACAGCAGCG TGGTGCGGCC AGTGGAAGAC   180
62  CACCGCCAGG TCGTGGAGGT CACCGTGGGC CTGCAGCTGA TACAGCTCAT CAATGTGGAT   240
63  GAAGTAAATC AGATCGTGAC AACCAATGTG CGTCTGAAAC AGCAATGGGT GGATTACAAC   300
64  CTAAAATGGA ATCCAGATGA CTATGGCGGT GTGAAAAAAA TTCACATTCC TTCAGAAAAG   360
65  ATCTGGCGCC CAGACCTTGT TCTCTATAAC AATGCAGATG GTGACTTTGC TATTGTCAAG   420
66  TTCACCAAAG TGCTCCTGCA GTACACTGGC CACATCACGT GGACACCTCC AGCCATCTTT   480
67  AAAAGCTACT GTGAGATCAT CGTCACCCAC TTTCCCTTTG ATGAACAGAA CTGCAGCATG   540
68  AAGCTGGGCA CCTGGACCTA CGACGGCTCT GTCGTGGCCA TCAACCCGGA AAGCGACCAG   600
69  CCAGACCTGA GCAACTTCAT GGAGAGCGGG GAGTGGGTGA TCAAGGAGTC CCGGGGCTGG   660
70  AAGCACTCCG TGACCTATTC CTGCTGCCCC GACACCCCCT ACCTGGACAT CACCTACCAC   720
71  TTCGTCATGC AGCGCCTGCC CCTCTACTTC ATCGTCAACG TCATCATCCC CTGCCTGCTC   780
72  TTCTCCTTCT TAACTGGCCT GGTATTCTAC CTGCCCACAG ACTCAGGGGA GAAGATGACT   840
73  CTGAGCATCT CTGTCTTACT GTCTTTGACT GTGTTCCTTC TGGTCATCGT GGAGCTGATC   900
74  CCCTCCACGT CCAGTGCTGT GCCCTTGATT GGAAAATACA TGCTGTTCAC CATGGTGTTC   960
75  GTCATTGCCT CCATCATCAT CACTGTCATC GTCATCAACA CACACCACCG CTCACCCAGC  1020
76  ACCCATGTCA TGCCCAACTG GGTGCGGAAG GTTTTTATCG ACACTATCCC AAATATCATG  1080
77  TTTTTCTCCA CAATGAAAAG ACCATCCAGA GAAAAGCAAG ACAAAAAGAT TTTTACAGAA  1140
78  GACATTGATA TCTCTGACAT TTCTGGAAAG CCAGGGCCTC CACCCATGGG CTTCCACTCT  1200
79  CCCCTGATCA AACACCCCGA GGTGAAAAGT GCCATCGAGG GCATCAAGTA CATCGCAGAG  1260
80  ACCATGAAGT CAGACCAGGA GTCTAACAAT GCGGCGGCAG AGTGGAAGTA CGTTGCAATG  1320
81  GTGATGGACC ACATACTCCT CGGAGTCTTC ATGCTTGTTT GCATCATCGG AACCCTAGCC  1380
82  GTGTTTGCAG GTCGACTCAT TGAATTAAAT CAGCAAGGAT GAGCAGAAAA TGAGCTGAGC  1440
83  TTAGCTCTGC CCTGGAACCT ACCAGAGCAG AGAAGGGCAG GAGAGGAAGA TTTGTCTACT  1500
84  TGCTCCACTC GCACTTATCA AACGTGTTAT ATTCCATACT TATTATTGAT GATAAGATTT  1560
85  ACCTTTATGT AAGTTTATGG CCTTGAAGTG TTTTCATATT GCTTCTCCCT TTAGTTCTGC  1620
86  TGTCTCCCTG AAGAGTGAAC CCTCTTTAGT AAATGAAACT AATCACT              1667
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87
88   (2) INFORMATION FOR SEQ ID NO:2:
89
90   (i) SEQUENCE CHARACTERISTICS:
91   (A) LENGTH: 457 amino acids
92   (B) TYPE: amino acid
93   (C) STRANDEDNESS: single
94   (D) TOPOLOGY: linear
95
96   (ii) MOLECULE TYPE: protein
97
98   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
99

INPUT SET: S27646.raw

100	Met	Glu	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Ser	Ala	Gly
101	1				5					10				15		
102	Leu	Val	Leu	Gly	Ser	Glu	His	Glu	Thr	Arg	Leu	Val	Ala	Lys	Leu	Phe
103			20					25					30			
104	Lys	Asp	Tyr	Ser	Ser	Val	Val	Arg	Pro	Val	Glu	Asp	His	Arg	Gln	Val
105			35				40						45			
106	Val	Glu	Val	Thr	Val	Gly	Leu	Gln	Leu	Ile	Gln	Leu	Ile	Asn	Val	Asp
107		50					55					60				
108	Glu	Val	Asn	Gln	Ile	Val	Thr	Thr	Asn	Val	Arg	Leu	Lys	Gln	Gln	Trp
109	65					70				75						80
110	Val	Asp	Tyr	Asn	Leu	Lys	Trp	Asn	Pro	Asp	Asp	Tyr	Gly	Gly	Val	Lys
111					85					90					95	
112	Lys	Ile	His	Ile	Pro	Ser	Glu	Lys	Ile	Trp	Arg	Pro	Asp	Leu	Val	Leu
113				100					105					110		
114	Tyr	Asn	Asn	Ala	Asp	Gly	Asp	Phe	Ala	Ile	Val	Lys	Phe	Thr	Lys	Val
115			115					120					125			
116	Leu	Leu	Gln	Tyr	Thr	Gly	His	Ile	Thr	Trp	Thr	Pro	Pro	Ala	Ile	Phe
117			130					135					140			
118	Lys	Ser	Tyr	Cys	Glu	Ile	Ile	Val	Thr	His	Phe	Pro	Phe	Asp	Glu	Gln
119	145					150					155					160
120	Asn	Cys	Ser	Met	Lys	Leu	Gly	Thr	Trp	Thr	Tyr	Asp	Gly	Ser	Val	Val
121					165					170					175	
122	Ala	Ile	Asn	Pro	Glu	Ser	Asp	Gln	Pro	Asp	Leu	Ser	Asn	Phe	Met	Glu
123				180					185					190		
124	Ser	Gly	Glu	Trp	Val	Ile	Lys	Glu	Ser	Arg	Gly	Trp	Lys	His	Ser	Val
125			195					200					205			
126	Thr	Tyr	Ser	Cys	Cys	Pro	Asp	Thr	Pro	Tyr	Leu	Asp	Ile	Thr	Tyr	His
127		210					215					220				
128	Phe	Val	Met	Gln	Arg	Leu	Pro	Leu	Tyr	Phe	Ile	Val	Asn	Val	Ile	Ile
129	225					230					235					240
130	Pro	Cys	Leu	Leu	Phe	Ser	Phe	Leu	Thr	Gly	Leu	Val	Phe	Tyr	Leu	Pro
131					245					250					255	
132	Thr	Asp	Ser	Gly	Glu	Lys	Met	Thr	Leu	Ser	Ile	Ser	Val	Leu	Leu	Ser
133				260					265					270		
134	Leu	Thr	Val	Phe	Leu	Leu	Val	Ile	Val	Glu	Leu	Ile	Pro	Ser	Thr	Ser
135			275					280					285			
136	Ser	Ala	Val	Pro	Leu	Ile	Gly	Lys	Tyr	Met	Leu	Phe	Thr	Met	Val	Phe
137		290					295					300				
138	Val	Ile	Ala	Ser	Ile	Ile	Ile	Thr	Val	Ile	Val	Ile	Asn	Thr	His	His
139	305					310					315					320
140	Arg	Ser	Pro	Ser	Thr	His	Val	Met	Pro	Asn	Trp	Val	Arg	Lys	Val	Phe
141					325					330					335	
142	Ile	Asp	Thr	Ile	Pro	Asn	Ile	Met	Phe	Phe	Ser	Thr	Met	Lys	Arg	Pro
143				340					345					350		
144	Ser	Arg	Glu	Lys	Gln	Asp	Lys	Lys	Ile	Phe	Thr	Glu	Asp	Ile	Asp	Ile
145			355					360					365			
146	Ser	Asp	Ile	Ser	Gly	Lys	Pro	Gly	Pro	Pro	Pro	Met	Gly	Phe	His	Ser
147			370					375					380			
148	Pro	Leu	Ile	Lys	His	Pro	Glu	Val	Lys	Ser	Ala	Ile	Glu	Gly	Ile	Lys
149	385					390					395					400
150	Tyr	Ile	Ala	Glu	Thr	Met	Lys	Ser	Asp	Gln	Glu	Ser	Asn	Asn	Ala	Ala
151					405					410					415	
152	Ala	Glu	Trp	Lys	Tyr	Val	Ala	Met	Val	Met	Asp	His	Ile	Leu	Leu	Gly

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/991,143*

INPUT SET: S27646.raw

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153                    420                   425                   430
154    Val Phe Met Leu Val Cys Ile Ile Gly Thr Leu Ala Val Phe Ala Gly
155            435                   440                   445
156    Arg Leu Ile Glu Leu Asn Gln Gln Gly
157        450                   455
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/991,143*

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Line	Error	Original Text